User Documentation 2
Backup Refuge Population Selection 3
Amphitrite Cross Selection Web Application 4
Backups 5
Fish Page 6
Recommend Crosses Workflow 10
Completed Crosses Page 14
User Management 17
User Settings 18

User Documentation

- Backup Refuge Population Selection
- Amphitrite Cross Selection Web Application

Backup Refuge Population Selection

The script to determine the backup refuge population is located in the amphitrite repository, located here (and can be downloaded from this location):

amphitrite/amphitrite/src/app/algorithms/backup_population_selection.py at main · adstruble/amphitrite

To execute the script, python must be installed (was run successfully in 3.10.4)

Execute this command:

```
python amphitrite/src/app/algorithms/backup_population_selection.py determine-parents-backup-tanks -r <full path to recommended crosses file>
```

To also indicate the number of tanks to use as backups, use the -t option (30 is the default). Example of the command with both options:

```
python amphitrite/src/app/algorithms/backup_population_selection.py determine-parents-backup-tanks -r ~/nereid51/data/recommeneded_crosses_2024.csv -t 31
```

The results of the running the script will be written to results.txt as better combination of tanks are found. The script is very long running although the results given within the first 20 minutes will likely be close the the optimum result, which can only be determined by running the script to completion. The results.txt file will be located in the same directory the python command is executed from.

To see the help text for the command, execute it with --help, see below:

```
% python amphitrite/src/app/algorithms/backup_population_selection.py determine-parents-backup-tanks --help
      Usage: backup_population_selection.py determine-parents-backup-tanks
                [OPTIONS]

        Determines the best combination of backup tanks to use, optimizing by number
        of distinct family groups represented. As input expects a
        recommended_crosses_file in csv format with the following columns:
        Date,Male,Male_Sibling_Group,Female,Female_Sibling_Group,<unused>,MFG While
        those are the expected columns, only the contents of the Male_Sibling_Group,
        Female_Sibling_Group and MFG are used.

      Options:
        -r, --recommended_crosses_file TEXT
                                        Full file path to recommended crosses CSV
                                        file  [required]
        -t, --tank_count INTEGER        The number of tanks that will be included as
                                        backups
        --help                          Show this message and exit.
```

Amphitrite Cross Selection Web Application

Using the Software

Fish Page

Managing the Software

Backups

Backups

Creation Policy

Snapshots of the volume the EC2 instance the application is running on are performed everyday. The snapshots are retained 7 days before being deleted.

Restore

In order to restore from a volume snapshot go the EC2 dashboard:

1. Select “Elastic Block Store”→Snapshots
2. Select the snapshot to restore from (most likely the latest)
3. Under Actions dropdown menu, select “Create Image from snapshot”
4. Give the image a name
5. Select Arm64 for architecture
6. Click “Create Image”
7. Go to Images→AMIs, Look for newly created image in list. You may have to hit the refresh button above the list in order for your new image to appear.
8. Select your new AMI
9. Click on “Launch Instance From AMI”
10. Name the server (e.g. Amphi Backup)
11. Select Instance type of t4g.medium
12. Under “Key pair (login)” select: amphitrite2.pem
13. Under “Common Security Groups” select: launch-wizard-2 sg-00287e918edd49912
14. Click “Launch Instance”
15. Once the instance is launched, find the Public IPv4 DNS in the Instance Summary for the new instance.
16. Connect to the new ECS instance:

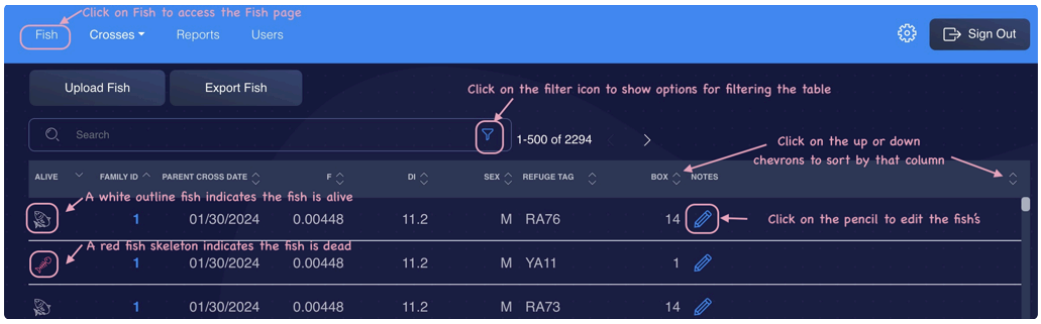
>ssh -i ~/.ssh/amphitrite2.pem.pem ec2-user@<public IPV4 DNS name>

17. On the EC2 instance start the docker project:

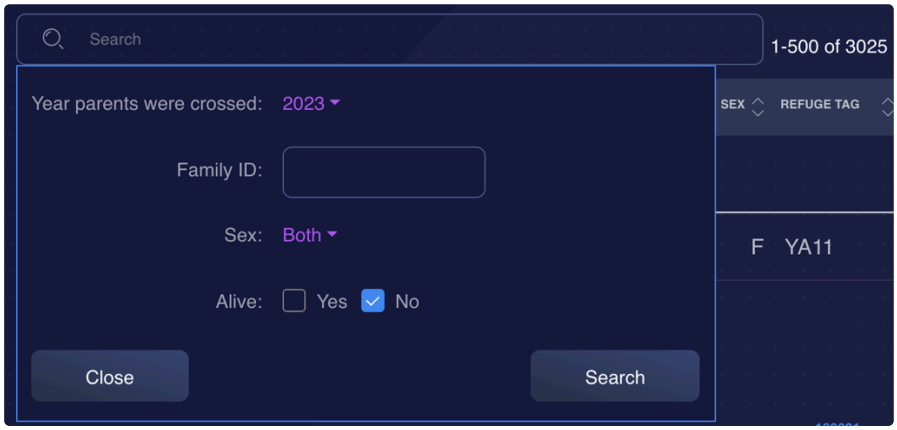
[ec2-user@<EC2 instance IP> ~]$ docker compose -f compose.yaml -p amphi up -d

Fish Page

Shows table with all the known fish as shown in the figure below:



When the page first loads, a default filter is set so that only *alive* fish whose parents were crossed in the previous year are included. To include other fish, click on the filter and adjust as necessary. The filter options are shown below.

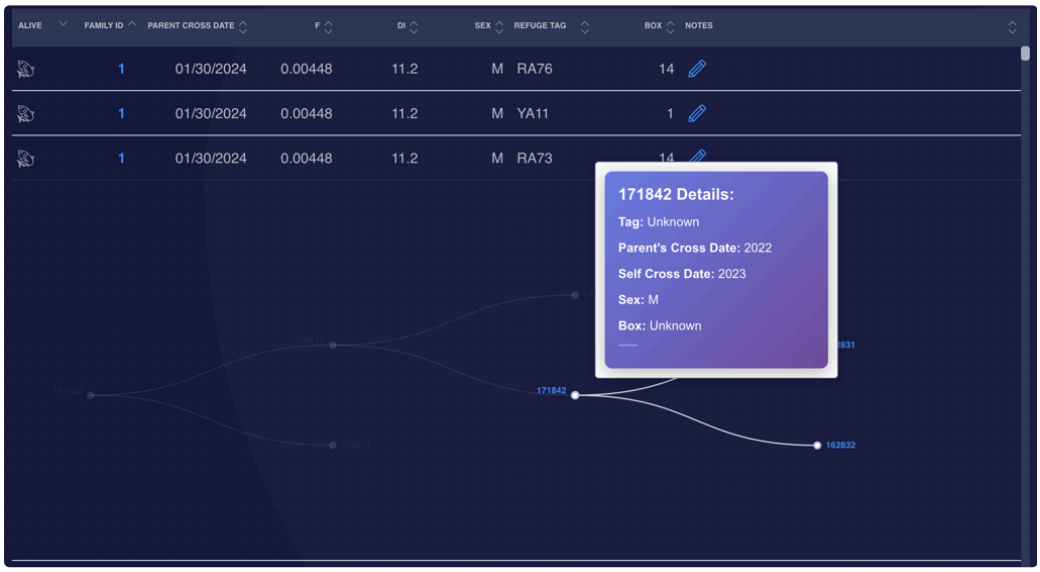


To include both dead and alive fish, check both the “Yes” and “No” boxes. To include only dead fish, select “No” and to select only alive fish, select “Yes”.

To filter the table, by other values, then those included in the Filter dialog, the “Search” bar above the table can be used. For example, it is possible to search for ‘YA’, which would result in a table, including all fish that pass the current filter and have tags beginning with ‘YA’.

Pedigree

The ancestry of any given fish can also be viewed in the Fish Table. In order to open the pedigree view for a fish, click on the Family Id. See image below:



In order to see information about a specific ancestor, mouse over that ancestor node. In order to see ancestors of an ancestor, click on the node and the pedigree graph will open an additional generation. To close an opened generation, click on the node again. The number displayed next to a node, is the generation ID of that fish.

Importing

In order to include new fish that the refuge has tagged, a master fish file that is a csv (i.e. values/columns are separated by commas) can be loaded. The file must contain the following columns in this order:

Notes,Tag,Sex,Family Id,Box,Allele Value 1,...,Allele Value 150

The ID Column is refuge tag, in the following formation: `RA73_2` where the _ and 1 or 2 following the underscore are ignored. If the fish is a 2 year old, a '2' should be prepended to the tag, i.e. in this case: 2RA73_2.

While the file is uploading, a spinner will show on the page. If the spinner fails to disappear after a few minutes, the page can be reloaded to see if the new fish have been uploaded. It is important not to begin selecting crosses until the import has complete. Once the “available fish” have been set in the “Request Crosses” page, newly imported fish will not be included in possible crosses.

Importing Updates

If a fish has had changes to its data and those changes are included in a new import, the fish will be updated to reflect the changes. In order to determine if a fish is the same as a fish that already exists in the software, the allele values of the fish are used to make matches. For

example, if a fish that is included in the import has allele values that all match a fish in the software, but their tags differ, the tag of the fish in the database will be updated to match the tag of the fish in the imported file.

Changes to Allele Values

Because the allele values are used to match fish, if changes need to made an existing fish's allele values, this *cannot* be done through the import feature. If the allele values are changed in the spreadsheet, no match will be found and an *additional* fish will be created. This will manifest as 2 fish with the same refuge tag (assuming the refuge tag also did not change). In order to change the allele values for existing fish, a different workflow must be followed <TO BE ADDED>.

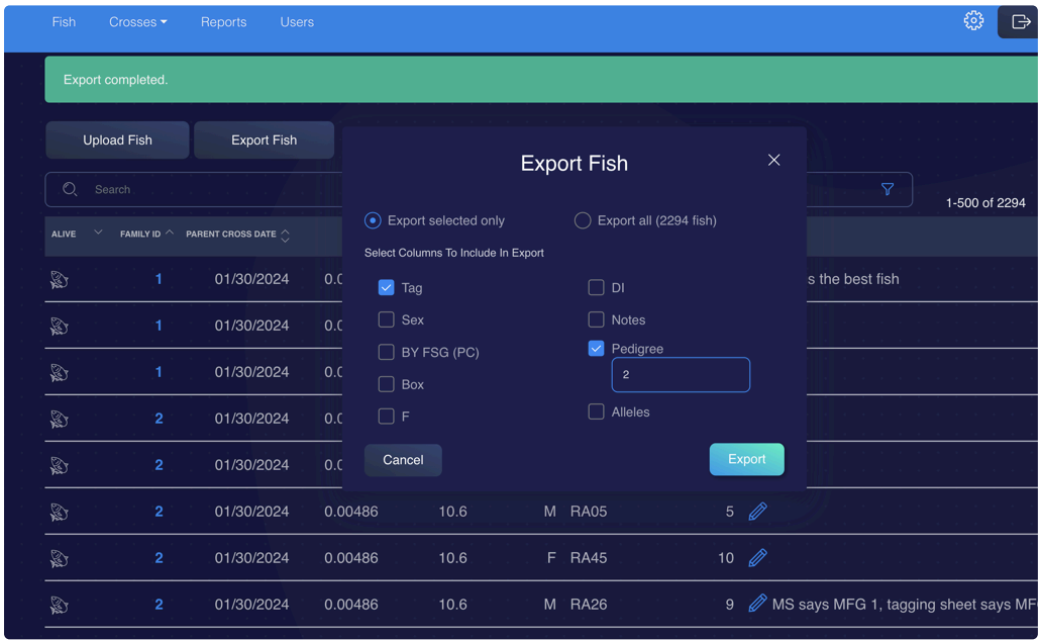
Exporting

If you want to export all the Fish that are currently included in the filter (all the fish currently shown in the table), click on the "Export Fish" button.

If you only want to export a subset of the fish currently showing in the table select by highlighting some part of all the rows you want to include. Then click "Export Fish".

In the Export Fish dialog that pops up, select the columns you want to export. If you want to export the pedigree. You also need to specify the number of generations you want to include in the pedigree. E.g. If you say 1, the current fish as well as it parents will be included in the exported pedigree. If you say 2, the current fish, its parents and its grandparents will be included in the exported pedigree.

In the example below, only the selected (by highlighting) rows will be included and each Fish's Tag and Pedigree will be included in the output. The pedigree will include 2 generations of ancestors.



Pedigree Output

The pedigree output for a fish is included in a single column with the following format:

<generation ID of fish> (Tag:<tag of fish> CrossDate:<Date parents of fish were crossed> Box:<Box of fish>) ⟵<generation number> – <generation ID of fish parent 1> (Tag:<tag of fish parent 1> CrossDate:<Date parents of fish parent 1 were crossed> Box:<Box of fish parent 1>) || <generation ID of fish parent 2> (Tag:<tag of fish parent 2> CrossDate:<Date parents of fish parent 2 were crossed> Box:<Box of fish parent 2>) ⟵<generation number> – <generation ID of ancestor>... etc.

Example of pedigree column value when exporting fish RA76:

193442 (Tag:RA76 CrossDate:2024-01-30 Box:14) ⟵1-- 180011 (Tag:YA33 CrossDate:2023 Box:6) || 180012 (Tag:OA09 CrossDate:2023 Box:6) ⟵2-- 170031 (CrossDate:2022) || 170032 (CrossDate:2022) || 171841 (CrossDate:2022) || 171842 (CrossDate:2022)

If any of the data is unknown (e.g. tag or box number) it is left out. If the full cross date is known it is included. Otherwise, only the cross year is shown.

Recommend Crosses Workflow

The **Recommend Crosses** page helps identify optimal crosses for maintaining a refuge population with minimal inbreeding. Users begin by specifying which fish are available for breeding. A table of possible crosses is then displayed, sorted so the *best* crosses appear first, based on the algorithm described in the Recommended Crosses Design . Users can select crosses for both refuge and supplementation populations. Recommended crosses can be **exported** to a CSV file, or the team performing the crosses can view them directly in the application. Completed crosses can be marked individually in the UI or **imported in bulk** from a CSV file through the Completed Crosses Page.

Workflow

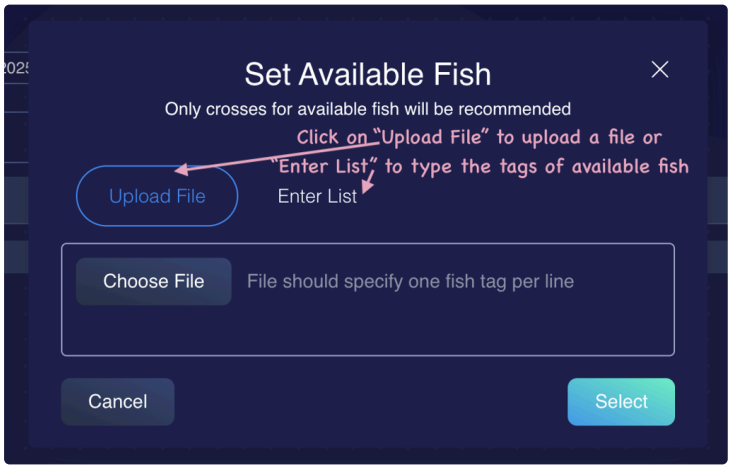
1. **Set available fish**
   - Users specify which fish are available for breeding.
   - Fish must already exist in the system (see Fish Page)
2. **View possible crosses**
   - A table of possible crosses is displayed.
   - Crosses are sorted so the *best* crosses appear first, as defined in the Cross Selection design.
3. **Select crosses**
   - Users select crosses to recommend for the refuge population.
   - Crosses can also be selected for a supplementation population.
4. **Communicate recommendations**
   - Recommended crosses can be exported to a CSV.
   - Alternatively, the team performing the crosses can log into the application directly.
5. **Record completed crosses**
   - Completed crosses can be marked individually in the UI.
   - Crosses can also be batch-uploaded via file (see Completed Crosses Page)

UI

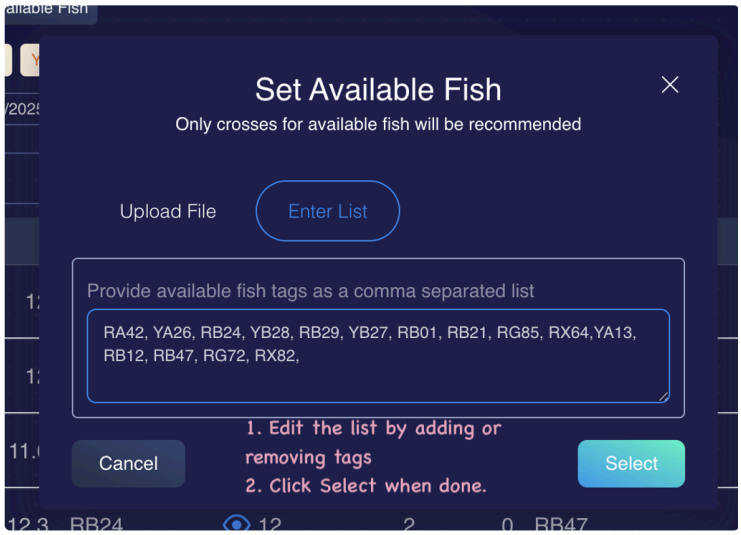
Navigating to Recommend Crosses

Setting Available Fish

- Click **Set Available Fish** to open the dialog.



- Fish tags may be:
  - Uploaded from a file (one tag per line), or
  - Entered manually.
- After upload, tags can be edited in the **Enter List** workflow.



Selecting Refuge and Supplementation Crosses

- The crosses table is initially sorted by:
  a. Inbreeding coefficient (**f**)
  b. Number of crosses already made for each family
- Selected crosses are automatically sorted to the top of the table.
- Users may change sort order (columns and ascending/descending).
- To assist selection:
  - A list of available females that have not yet been crossed is displayed at the top of the page.
  - Clicking the **eye icon** next to a family ID opens details showing all crosses already made with that family.
  - Current **population f values** (for both refuge and supplementation) are shown in the upper-right corner. These values update dynamically as crosses are selected.

Exporting Selected Crosses

- After selection, click **Export Selected Crosses** to download a CSV.
- The file contains two lists (refuge and supplementation), each including:
  - Female tags
  - Female family
  - Male tags
  - Male family
  - f (inbreeding coefficient)
  - Crosses completed for the female's family
  - Crosses completed for the male's family

Completing Crosses

- To mark a cross as completed:
  a. Set the **completion date** above the table.
  b. Check **Cross Completed** for each relevant cross.
- Alternatively, upload a file of completed crosses through the Completed Crosses Page

Completed Crosses Page

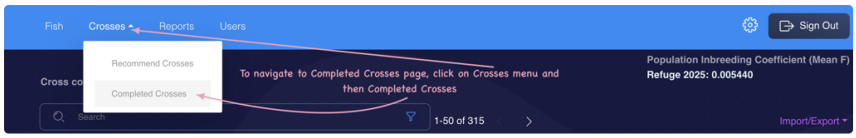
The **Completed Crosses** page provides access to all completed crosses for both refuge and supplementation populations. Populations can be viewed by **year** and **population type**. The page displays the population inbreeding coefficient (Mean F) along with a table of all completed crosses, regardless of whether offspring resulted.

The table includes controls for **searching, filtering, and sorting**, and dropdown menus allow users to switch between year and population type. Completed crosses can be **imported in bulk** from a CSV file. Data can also be **exported** in two formats:

- **Pair cross export** – one cross per line, with both parents shown.
- **Parentage export** – one parent per line (two lines per cross), with allele data and family IDs for both the parent and its offspring.

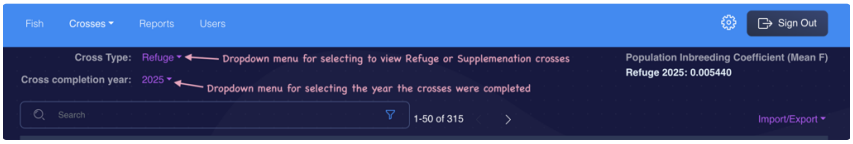
UI

Navigating to Completed Crosses



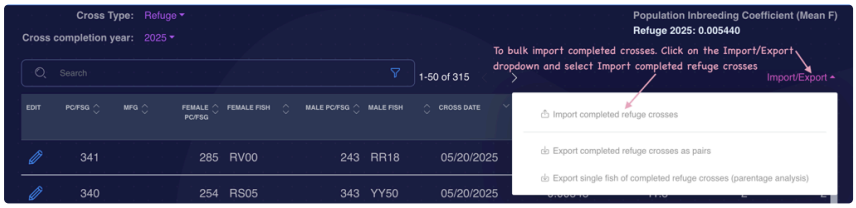
Viewing by Population and Year

Users can choose which population type (refuge or supplementation) and which cross year to view using the dropdown menus at the top of the page.



Importing Completed Crosses

To bulk import completed crosses, open the **Import/Export** dropdown and select **Import Completed <Refuge/Supplementation> Crosses**. The population type of the import is determined by the current view (refuge or supplementation).



The import file must be a CSV with the following required columns:

- `Date`
- `Male`

- `Female`
- `<any text>BY<any text>FSG<any text>`

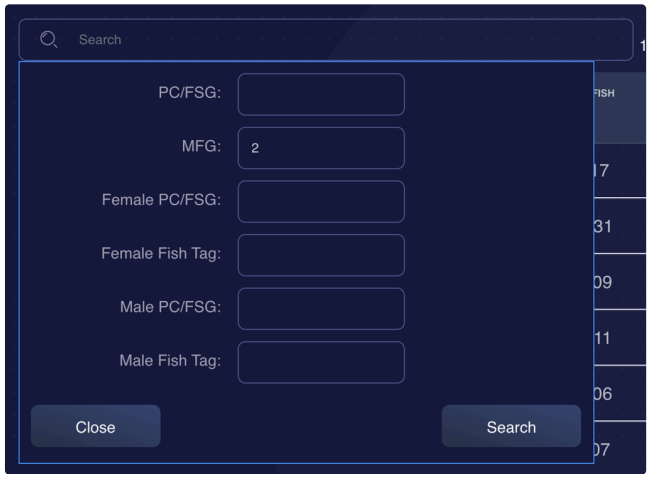
A `Comment` column may also be included. If present, values in this column will be added as a **Note** on the completed cross. Columns may appear in any order, but a **header row is required**. Other columns may be included but will be ignored.

Viewing Completed Crosses

By default, the table shows all completed crosses for the selected year and population type. The table can be **sorted, filtered, and searched** (see figure below).

- **Free text search** matches rows containing any of the entered text.
- **Filters** require exact matches. For example:
  - If *Female Fish Tag* is set to `RV`, no results will appear.
  - If set to `RV44`, the table will display the cross where the female parent is `RV44`.

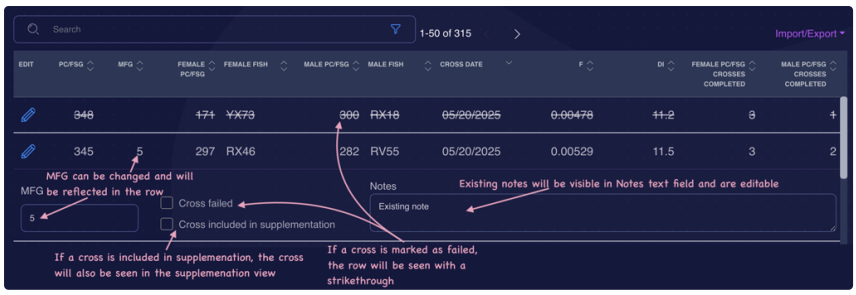
When clicking the filter icon, the filter dialog appears (see figure below).



Editing Completed Crosses

To edit a cross, click the **pencil icon** in the row. This opens a panel below the row with editable fields.

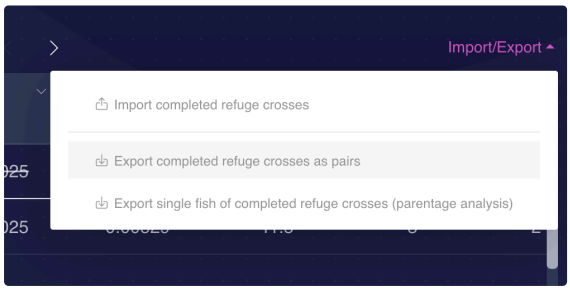
- Click the pencil again to close the panel.



Exporting Crosses

From the **Import/Export** dropdown, two export options are available. Both exports include only the crosses currently visible in the table (i.e., filters and searches are applied).

- **Completed <Refuge/Supplementation> Crosses as Pairs** – one cross per line, both parents listed. Details of the cross (e.g. f, DI, etc) are included.
- **Single Fish of Completed <Refuge/Supplementation> Crosses (Parentage Analysis)** – one parent per line, two lines per cross, genetic data for the parent is included.



User Management

To add, remove, or disable users, click **Users** in the top navigation bar.

Adding Users

When a new user is added, their account will be created with the specified username and a default password of `pass`. Upon first login, the user must change their password via the [User Settings](#) page.

User Associations

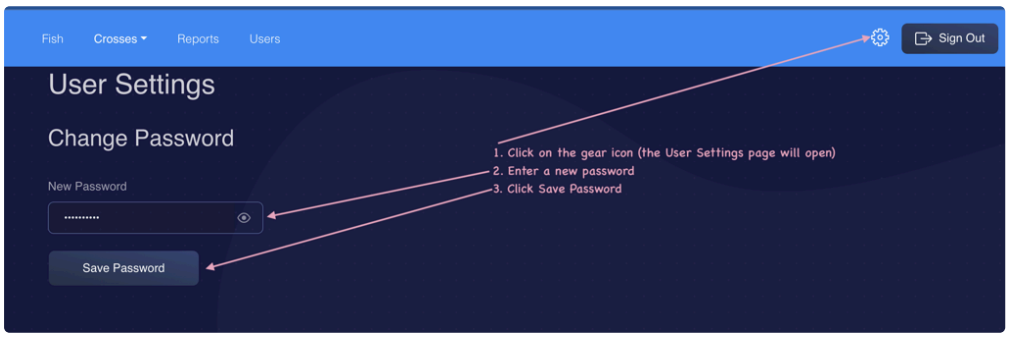
Every action in the system is tied to a specific user (e.g., adding fish, selecting possible crosses, recording completed crosses, or editing crosses). If a user is deleted, their past actions will remain in the system, but no new actions can be associated with that account—even if a new user is later created with the same username.

Disabling vs. Deleting Users

If you want to prevent a user from logging in but may need to restore access later, it is best to **disable** the user rather than delete them.

User Settings

Currently, the only available user setting is the **password**.

To change your password:

1. Click the **gear icon** in the upper-right corner of the page.
2. Enter your new password.
3. Click **Save Password**.